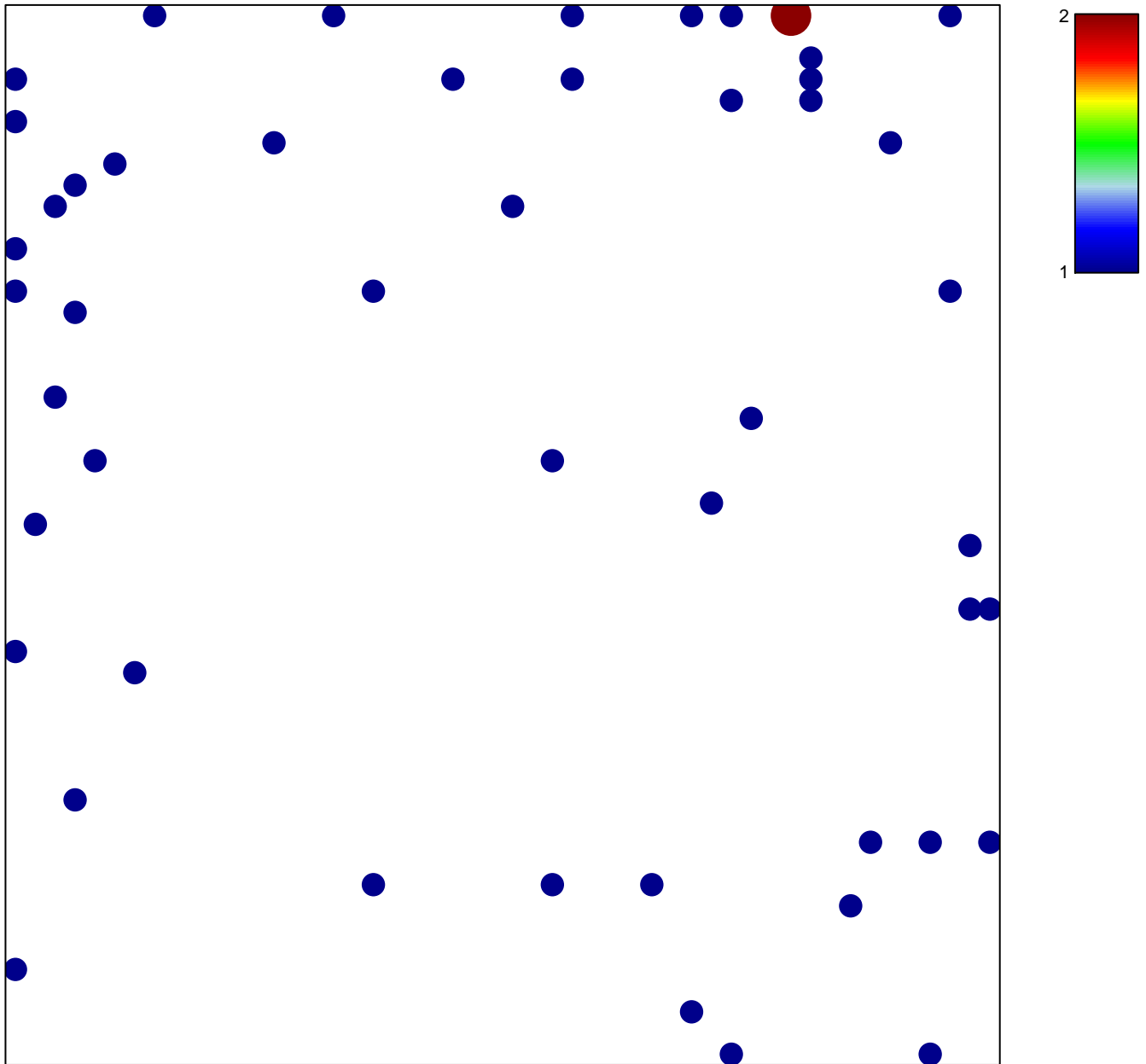
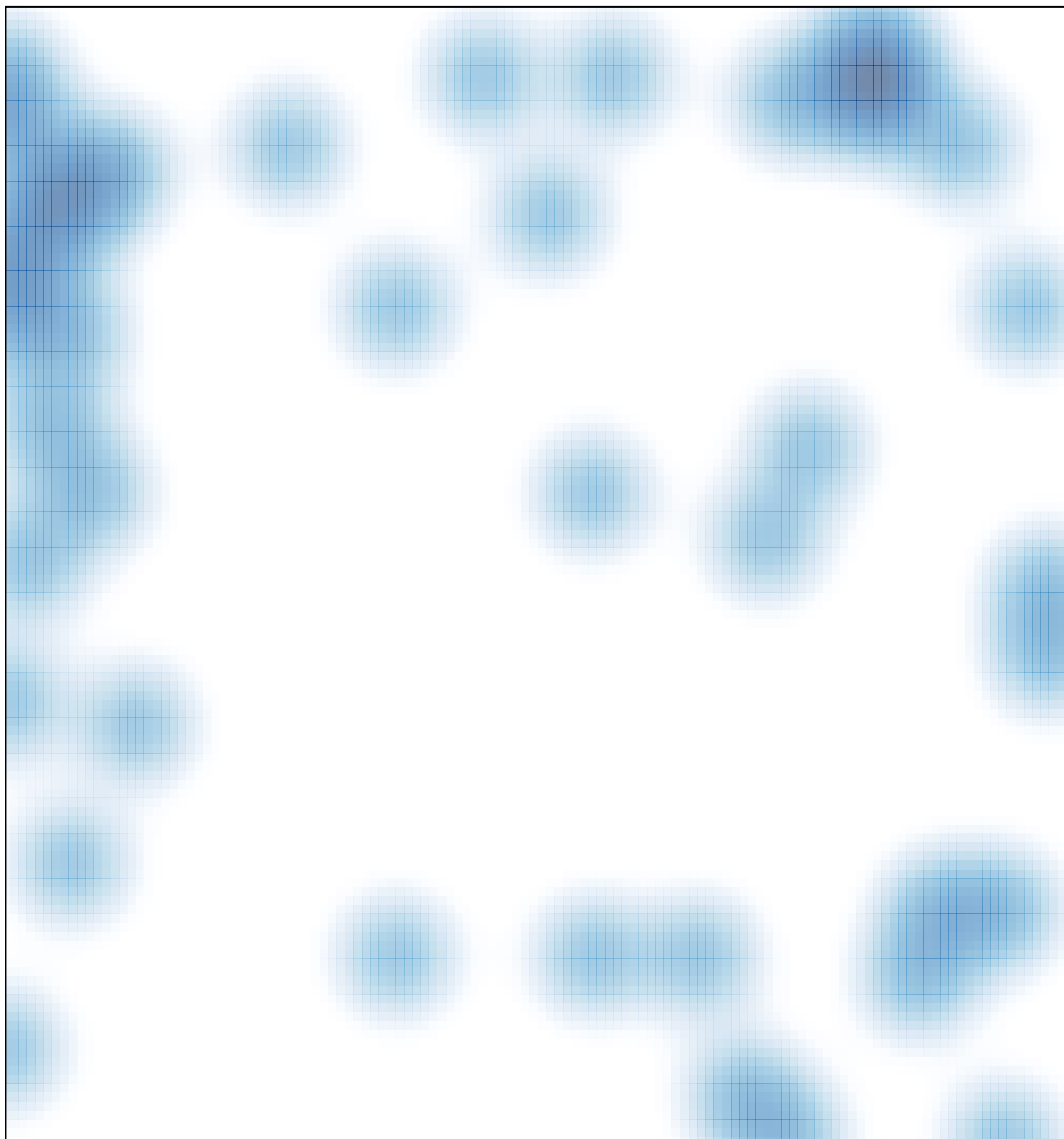


# WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotG



# features = 50  
chi-square p = 0.8

# WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotG



# features = 50 , max = 2